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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/695,795

DATE: 11/09/2000  
 TIME: 11:41:58

Input Set : A:\JHU1650-2.ST25.txt  
 Output Set: N:\CRF3\11092000\I695795.raw

3 <110> APPLICANT: JOHN HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 4 Jeffrey, Rothstein  
 5 Jackson, Mandy  
 6 Lin, Glenn  
 7 Law, Robert  
 8 Orlow, Irina  
 10 <120> TITLE OF INVENTION: GLUTAMATE TRANSPORTER ASSOCIATED PROTEINS AND METHODS OF USE THEREOF  
 12 <130> FILE REFERENCE: JHU1650-2  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/695,795  
 C--> 14 <141> CURRENT FILING DATE: 2000-10-23  
 14 <150> PRIOR APPLICATION NUMBER: 60/161,007  
 15 <151> PRIOR FILING DATE: 1999-10-23  
 17 <160> NUMBER OF SEQ ID NOS: 22  
 19 <170> SOFTWARE: PatentIn version 3.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 7240  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Rattus  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)..(7164)  
 30 <400> SEQUENCE: 1  
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 32 Met Ser Thr Ile Ser Pro Thr Asp Phe Asp Ser Leu Glu Ile Gln  
 33 1 5 10 15  
 35 ggc cag tac agt gac atc aac aac cgc tgg gac ctg ccc gac tca gat 96  
 36 Gly Gln Tyr Ser Asp Ile Asn Asn Arg Trp Asp Leu Pro Asp Ser Asp  
 37 20 25 30  
 39 tgg gac aat gac agc agt tca gcc cgc ctc ttt gag agg tcc aya att 144  
 40 Trp Asp Asn Asp Ser Ser Ala Arg Leu Phe Glu Arg Ser Arg Ile  
 41 35 40 45  
 43 aag gcc ctg gca gat gag cga gaa gcc gtg cag aag aaa acc ttc acc 192  
 44 Lys Ala Leu Ala Asp Glu Arg Ala Val Gln Lys Lys Thr Phe Thr  
 45 50 55 60  
 47 aag tgg gtg aac tcc cac ctg gcc cgg gtg aca tgc cgg gtg gga gac 240  
 48 Lys Trp Val Asn Ser His Leu Ala Arg Val Thr Cys Arg Val Gly Asp  
 49 65 70 75 80  
 51 ctg tac agc ctg cgg gac ggg cgc aac ctc ctc agg ctc ctg gag 288  
 52 Leu Tyr Ser Asp Leu Arg Asp Gly Arg Asn Leu Leu Arg Leu Leu Glu  
 53 85 90 95  
 55 gtg ctc tct gga gag acc ctg cca aaa ccc acc aag ggc cgg atg cgg 336  
 56 Val Leu Ser Gly Glu Thr Leu Pro Lys Pro Thr Lys Gly Arg Met Arg  
 57 100 105 110  
 59 att cac tgc ctg gag aat gtc gac aaa gca ctg cag ttc ctg aag gag 384  
 60 Ile His Cys Leu Glu Asn Val Asp Lys Ala Leu Gln Phe Leu Lys Glu  
 61 115 120 125  
 63 cag aag gtg cac ctg gaa aac atg ggc tcc cac gac att gtg gat ggg 432

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64	Gln	Lys	Val	His	Leu	Glu	Asn	Met	Gly	Ser	His	Asp	Ile	Val	Asp	Gly	
65	130				135				140								
67	aac	cac	cgt	ctg	acc	ctt	ggg	cta	gtg	tgg	acc	atc	atc	ctc	cga	ttt	480
68	Asn	His	Arg	Leu	Thr	Leu	Gly	Leu	Val	Trp	Thr	Ile	Ile	Leu	Arg	Phe	
69	145				150				155							160	
71	cag	atc	caa	gac	atc	agt	gtg	gag	aca	gaa	gac	aac	aag	gag	aag	aag	528
72	Gln	Ile	Gln	Asp	Ile	Ser	Val	Glu	Thr	Glu	Asp	Asn	Lys	Glu	Lys	Lys	
73									165		170				175		
75	tca	gcc	aag	gat	gcc	ctg	ctg	tgg	tgc	cag	atg	aag	act	gca	ggg		576
76	Ser	Ala	Lys	Asp	Ala	Leu	Leu	Leu	Trp	Cys	Gln	Met	Lys	Thr	Ala	Gly	
77									180		185				190		
79	tat	ccc	aat	gtc	aat	gtg	cac	aac	ttt	acc	acc	agt	tgg	aga	gat	ggg	624
80	Tyr	Pro	Asn	Val	Asn	Val	His	Asn	Phe	Thr	Thr	Ser	Trp	Arg	Asp	Gly	
81									195		200				205		
83	ctg	gcc	ttt	aat	gcc	att	gtg	cac	aaa	cac	cgg	cca	gac	ctg	tgg	gat	672
84	Leu	Ala	Phe	Asn	Ala	Ile	Val	His	Lys	His	Arg	Pro	Asp	Leu	Leu	Asp	
85									210		215				220		
87	ttt	gag	tcc	ctg	aag	aag	tgt	aac	gca	cac	tac	aat	ctg	cag	aat	gtc	720
88	Phe	Glu	Ser	Leu	Lys	Lys	Cys	Asn	Ala	His	Tyr	Asn	Leu	Gln	Asn	Ala	
89									225		230				235		240
91	tcc	aat	ctg	gct	gaa	aag	gaa	ctt	ggc	ctg	acg	aag	ctc	ctg	gat	cct	768
92	Phe	Asn	Leu	Ala	Glu	Lys	Glu	Leu	Gly	Leu	Thr	Lys	Leu	Leu	Asp	Pro	
93									245		250				255		
95	gaa	gat	gtg	aac	gtt	gac	caa	ccc	gat	gag	aag	tcc	atc	atc	acc	tac	816
96	Glu	Asp	Val	Asn	Val	Asp	Gln	Pro	Asp	Glu	Lys	Ser	Ile	Ile	Thr	Tyr	
97									260		265				270		
99	gtg	gcc	act	tac	tac	cac	tac	tcc	aat	gtg	aag	gtt	gcc	ctg	gtc	gtg	864
100	Val	Ala	Thr	Tyr	Tyr	His	Tyr	Phe	Ser	Lys	Met	Lys	Ala	Leu	Ala	Val	
101									275		280				285		
103	gaa	ggc	aaa	agg	att	ggc	aag	gtc	ctg	gac	cat	gcc	atg	gag	gca	gaa	912
104	Glu	Gly	Lys	Arg	Ile	Gly	Lys	Val	Leu	Asp	His	Ala	Met	Glu	Ala	Glu	
105									290		295				300		
107	cac	ctg	gtt	gag	aaa	tat	gag	tcc	ctg	gcc	tct	gaa	ctg	ctg	cag	tgg	960
108	His	Leu	Val	Glu	Lys	Tyr	Glu	Ser	Leu	Ala	Ser	Glu	Leu	Leu	Gln	Trp	
109									305		310				315		320
111	atc	gag	caa	acg	att	ggg	acc	ttc	aat	gac	cga	cag	ctg	gcc	acc	tcc	1008
112	Ile	Glu	Gln	Thr	Ile	Gly	Thr	Phe	Asn	Asp	Arg	Gln	Leu	Ala	Asn	Ser	
113									325		330				335		
115	ctg	agt	ggc	gtc	cag	aac	cag	ctg	cag	tct	aat	tcc	tac	cgc	acg		1056
116	Leu	Ser	Gly	Val	Gln	Asn	Gln	Leu	Gln	Ser	Phe	Asn	Ser	Tyr	Arg	Thr	
117									340		345				350		
119	gtg	gag	aag	cca	ccc	aag	ttc	aca	gag	aaa	ggg	aac	ttg	gag	gtg	ttg	1104
120	Val	Glu	Lys	Pro	Pro	Lys	Phe	Thr	Glu	Lys	Gly	Asn	Leu	Glu	Val	Leu	
121									355		360				365		
123	ctc	tcc	acc	atc	cag	agt	aag	ctg	cgg	gcc	aac	aac	cag	aaa	gtc	tac	1152
124	Leu	Phe	Thr	Ile	Gln	Ser	Lys	Leu	Arg	Ala	Asn	Asn	Gln	Lys	Val	Tyr	
125									370		375				380		
127	aca	cca	cgc	gaa	ggc	cgg	ctc	atc	tgc	gac	atc	aac	aag	gcc	tgg	gag	1200
128	Thr	Pro	Arg	Glu	Gly	Arg	Leu	Ile	Ser	Asp	Ile	Asn	Lys	Ala	Trp	Glu	

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129	385	390	395	400	
131	cgg cta gag aaa gcc gaa cat gag cga gag ctg gcc cgc acg gag				1248
132	Arg Leu Glu Lys Ala Glu His Glu Arg Glu Leu Ala Leu Arg Thr Glu				
133	405	410	415		
135	ctg atc cgc cag gag aag ctg gag caa ctg gct gct cgc ttc gac cgc				1296
136	Leu Ile Arg Gln Glu Lys Leu Glu Gln Leu Ala Ala Arg Phe Asp Arg				
137	420	425	430		
139	aag gct gcc att cgg gag acc tgg ctc agt gag aac caq cgc ctc gtc				1344
140	Lys Ala Ala Met Arg Glu Thr Trp Leu Ser Glu Asn Gln Arg Leu Val				
141	435	440	445		
143	tcc cag gac aac ttt ggc ctg gag ctg qca gca gtg gag gca gca gtg				1392
144	Ser Gln Asp Asn Phe Gly Leu Glu Leu Ala Ala Val Glu Ala Ala Val				
145	450	455	460		
147	cgg aag cat gaa gcc att gag aca gac att gtg gcc tac agc ggc cgg				1440
148	Arg Lys His Glu Ala Ile Glu Thr Asp Ile Val Ala Tyr Ser Gly Arg				
149	465	470	475	480	
151	gtg caa gcg gtg gac gcc gta gcc gca gaa ctg gcc gct gag cat tac				1488
152	Vai Gln Ala Vai Asp Ala Val Ala Ala Glu Leu Ala Ala Glu His Tyr				
153	485	490	495		
155	cat gac att aag cgc att gcg qcg cgg cag aac aac gtg gcc cgg ctc				1536
156	His Asp Ile Lys Arg Ile Ala Ala Arg Gln Asn Asn Val Ala Arg Leu				
157	500	505	510		
159	tgg gac ttc tta cga gag atg gtg gcc gcc cgt gag cgg ctc ctt				1584
160	Trp Asp Phe Leu Arg Glu Met Val Ala Ala Arg Arg Glu Arg Leu Leu				
161	515	520	525		
163	ctc aac ctg gag ctg cag aag gtg ttt cag gac ctg ctc tac ctc atg				1632
164	Leu Asn Leu Glu Leu Gln Lys Val Phe Gln Asp Leu Leu Tyr Leu Met				
165	530	535	540		
167	gac tgg atg gca gag atg aag ggc cgg ctg cag tct cag gac cta ggc				1680
168	Asp Trp Met Ala Glu Met Lys Gly Arg Leu Gln Ser Gln Asp Leu Gly				
169	545	550	555	560	
171	aag cat ctg gct gga gtg gaa gat cta ctg caa cta cac gaa ctg gtg				1728
172	Lys His Leu Ala Gly Val Glu Asp Leu Leu Gln Leu His Glu Leu Val				
173	565	570	575		
175	gag gcg gac att gca gtt cag gct gag agg gtg cga gcg gtc agc gcc				1776
176	Glu Ala Asp Ile Ala Val Gln Ala Glu Arg Val Arg Ala Val Ser Ala				
177	580	585	590		
179	tct gcc ctg cgc ttc tgc gac cca ggg aaa gag tat aqa cct tgc ggc				1824
180	Ser Ala Leu Arg Phe Cys Asp Pro Gly Lys Glu Tyr Arg Pro Cys Gly				
181	595	600	605		
183	ccg cag cta gtg tca gag agg gta gcc act ctg gag cag agc tat gag				1872
184	Pro Gln Leu Val Ser Glu Arg Val Ala Thr Leu Glu Gln Ser Tyr Glu				
185	610	615	620		
187	gcc ctg tgc gaa ttg gca gca act cga agg gcc cga ctg gaa gag tcc				1920
188	Ala Leu Cys Glu Leu Ala Ala Thr Arg Arg Ala Arg Leu Glu Glu Ser				
189	625	630	635	640	
191	cgt cgt ctc tgg agg ttc ctc tgg gaa gtg ggt gag gcc gag gcc tgg				1968
192	Arg Arg Leu Trp Arg Phe Leu Trp Glu Val Gly Glu Ala Glu Ala Trp				
193	645	650	655		

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195	gtt	cgg	gag	cag	cag	cac	ctc	ctg	gcc	tca	gtc	gag	aca	ggc	cgg	gac		2016	
196	Val	Arg	Glu	Gln	Gln	His	Leu	Leu	Ala	Ser	Ala	Glu	Thr	Gly	Arg	Asp			
197							660				665					670			
199	ctg	act	ggt	gtc	ctc	cgc	ctg	ctc	aat	aag	cac	aca	gcc	cta	cgg	ggt		2064	
200	Leu	Thr	Gly	Val	Leu	Arg	Leu	Leu	Asn	Lys	His	Thr	Ala	Leu	Arg	Gly			
201							675				680					685			
203	qag	atg	agt	ggc	cgc	ctg	ggg	ccc	ctg	aag	ctc	acc	ctg	gaa	caa	ggt		2112	
204	Glu	Met	Ser	Gly	Arg	Leu	Gly	Pro	Leu	Lys	Leu	Thr	Leu	Glu	Gln	Gly			
205							690				695					700			
207	cag	cag	tta	gtt	gcc	gag	ggc	cac	cct	gga	gtc	aac	caa	gcc	tca	acc		2160	
208	Gln	Gln	Leu	Val	Ala	Glu	Gly	His	Pro	Gly	Ala	Asn	Gln	Ala	Ser	Thr			
209							705				710					715		720	
211	cgt	gca	gca	gag	ctc	cag	gcc	cag	tgg	gag	cga	cta	gaa	gcc	ctg	gcc		2208	
212	Arg	Ala	Ala	Glu	Leu	Gln	Ala	Gln	Trp	Glu	Arg	Leu	Glu	Ala	Leu	Ala			
213							725				730					735			
215	qag	gag	cga	gcc	cag	cgg	cta	gca	cag	gtc	gcc	agc	ctc	tac	cag	ttc		2256	
216	Glu	Glu	Arg	Ala	Gln	Arg	Leu	Ala	Gln	Ala	Ala	Ser	Leu	Tyr	Gln	Phe			
217							740				745					750			
219	cag	gca	gat	gcc	aat	gac	atg	gag	gtc	tgg	tgg	gtg	gac	gca	cta	cgc		2304	
220	Gln	Ala	Asp	Ala	Asn	Asp	Met	Glu	Ala	Trp	Leu	Val	Asp	Ala	Leu	Arg			
221							755				760					765			
223	ctg	gta	tct	atc	cgc	cct	gag	gtt	ggg	cac	gat	gag	tcc	tcc	acg	cag	gcc		2352
224	Leu	Val	Ser	Ser	Pro	Glu	Val	Gly	His	Asp	Glu	Phe	Ser	Thr	Gln	Ala			
225							770				775					780			
227	ctg	gcc	agg	cag	cac	agg	gcc	ctt	gag	gag	atc	cga	gcc	cac	cgg			2400	
228	Leu	Ala	Arg	Gln	His	Arg	Ala	Leu	Glu	Glu	Glu	Ile	Arg	Ala	His	Arg			
229							785				790					795		800	
231	cct	aca	ctg	gat	gcc	tgg	agg	gag	cag	gtc	gca	gcc	ctg	cca	cct	gca		2448	
232	Pro	Thr	Leu	Asp	Ala	Leu	Arg	Glu	Gln	Ala	Ala	Ala	Leu	Pro	Pro	Ala			
233							805				810					815			
235	ctg	atc	gac	cac	aca	cct	gag	gtt	ggc	agg	gtt	ccc	act	ctg	gag	cag		2496	
236	Leu	Ser	His	Thr	Pro	Glu	Val	Gln	Gly	Arg	Val	Pro	Thr	Leu	Glu	Gln			
237							820				825					830			
239	cac	tat	gag	gag	ctg	cag	gcc	cgg	gca	ggt	gag	cgt	gca	cga	gcc	ctg		2544	
240	His	Tyr	Glu	Glu	Leu	Gln	Ala	Arg	Ala	Gly	Glu	Arg	Ala	Arg	Ala	Leu			
241							835				840					845			
243	gaa	gca	gcc	ctg	cgc	tcc	tat	acc	atg	ctc	atc	gag	gcc	ggg	gct	tgt		2592	
244	Glu	Ala	Ala	Leu	Ala	Phe	Tyr	Thr	Met	Leu	Ser	Glu	Ala	Gly	Ala	Cys			
245							850				855					860			
247	ggg	ctc	tgg	gtt	gta	gag	gag	aag	gag	cag	tgg	ctc	aac	ggg	ctg	gcc	cta		2640
248	Gly	Ieu	Trp	Val	Glu	Glu	Lys	Glu	Gln	Trp	Leu	Asn	Gly	Leu	Ala	Leu			
249							865				870					875		880	
251	cct	gag	cgc	ctg	gag	gac	ccg	gag	gtt	gtc	caa	cag	agg	ttt	gag	acc		2688	
252	Pro	Glu	Arg	Leu	Glu	Asp	Pro	Glu	Val	Val	Gln	Gln	Arg	Phe	Glu	Thr			
253							885				890					895			
255	tta	gag	ccc	gaa	atg	aac	gcc	ctg	gct	gca	cgg	att	act	gtt	gtc	agt		2736	
256	Leu	Glu	Pro	Glu	Met	Asn	Ala	Leu	Ala	Ala	Arg	Ile	Thr	Ala	Val	Ser			
257							900				905					910			
259	gac	ata	gtt	gag	cag	tgg	ctg	aag	gcc	agt	cca	cca	ggc	aag	yac	cyc		2784	

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260	Asp	Ile	Ala	Glu	Gln	Leu	Leu	Lys	Ala	Ser	Pro	Pro	Gly	Lys	Asp	Arg
261		915		920		925										
263	atc	att	ggc	acc	cag	cag	cag	ctc	aac	caa	agg	tgg	cag	cag	ttc	agg
264	Ile	Ile	Gly	Thr	Gln	Glu	Gln	Leu	Asn	Gln	Arg	Trp	Gln	Gln	Phe	Arg
265		930		935		940										
267	tcc	ctg	gca	ggt	ggc	aaa	aag	yca	gct	ctg	aca	tca	gcc	ctg	agc	atc
268	Ser	Leu	Ala	Gly	Gly	Lys	Lys	Ala	Ala	Leu	Thr	Ser	Ala	Leu	Ser	Ile
269	945		950		955		960									
271	cag	aat	tac	cac	cta	gag	tgc	aca	gag	acc	cag	gcc	tgg	atg	aga	gaa
272	Gln	Asn	Tyr	His	Leu	Glu	Cys	Thr	Glu	Thr	Gln	Ala	Trp	Met	Arg	Glu
273		965		970		975										
275	aag	acc	aag	gtc	att	gag	tct	acc	cag	qac	cta	ggc	aat	gat	cta	gct
276	Lys	Thr	Lys	Val	Ile	Glu	Ser	Thr	Gln	Asp	Leu	Gly	Asn	Asp	Leu	Ala
277		980		985		990										
279	ggg	gtg	ctg	gcc	ctg	cag	cgg	aaa	ctg	gca	ggc	act	gag	aga	gat	ctg
280	Gly	Val	Leu	Ala	Leu	Gln	Arg	Lys	Leu	Ala	Gly	Thr	Glu	Arg	Asp	Leu
281		995		1000		1005										
283	gaa	gcc	atc	tct	gcc	cgg	gtg	ggg	gtg	acc	caa	gag	gca	aat		3069
284	Glu	Ala	Ile	Ser	Ala	Arg	Val	Gly	Glu	Leu	Thr	Gln	Glu	Ala	Asn	
285		1010		1015		1020										
287	gct	ttg	gct	gtt	ggg	cac	cca	gcc	caa	gcc	cct	gcc	atc	aac	aca	3114
288	Ala	Leu	Ala	Ala	Gly	His	Pro	Ala	Gln	Ala	Pro	Ala	Ile	Asn	Thr	
289		1025		1030		1035										
291	cgg	ctt	gga	gag	gtt	caa	act	gga	tgg	gag	gat	ctt	cgg	gca	acc	3159
292	Arg	Leu	Gly	Glu	Val	Gln	Thr	Gly	Trp	Glu	Asp	Leu	Arg	Ala	Thr	
293		1040		1045		1050										
295	atg	agg	cgg	aga	gaa	gag	tcc	ctg	gtt	gag	gct	cga	cgg	ctg	caa	3204
296	Met	Arg	Arg	Arg	Glu	Glu	Ser	Leu	Gly	Glu	Ala	Arg	Arg	Leu	Gln	
297		1055		1060		1065										
299	gat	ttc	ctg	cgc	agc	tta	gat	gac	ttc	cag	gcc	tgg	cta	ggc	cgc	3249
300	Asp	Phe	Leu	Arg	Ser	Leu	Asp	Asp	Phe	Gln	Ala	Trp	Leu	Gly	Arg	
301		1070		1075		1080										
303	aca	cag	act	gct	gtt	gcc	tct	gag	gaa	gga	cca	gcc	acc	ctt	cca	3294
304	Thr	Gln	Thr	Ala	Val	Ala	Ser	Glu	Glu	Gly	Pro	Ala	Thr	Leu	Pro	
305		1085		1090		1095										
307	gag	gca	gaa	gcc	ctc	tta	gcc	cag	cat	gca	gct	ctg	cgg	gga	gag	3339
308	Glu	Ala	Glu	Ala	Leu	Leu	Ala	Gln	His	Ala	Ala	Leu	Arg	Gly	Glu	
309		1100		1105		1110										
311	gtg	gag	aga	gcc	cag	agc	gag	tac	agc	cgc	ctc	agg	acc	ttg	ggc	3384
312	Val	Glu	Arg	Ala	Gln	Ser	Glu	Tyr	Ser	Arg	Leu	Arg	Thr	Leu	Gly	
313		1115		1120		1125										
315	gag	gag	gtg	acc	aga	gac	cag	gct	gat	ccc	caa	tgc	ctc	ttc	ctc	3429
316	Glu	Glu	Val	Thr	Arg	Asp	Gln	Ala	Asp	Pro	Gln	Cys	Leu	Phe	Leu	
317		1130		1135		1140										
319	aga	cag	agg	ctg	gaa	gcc	ctt	gga	acc	ggc	tgg	gag	gag	ctg	ggt	3474
320	Arg	Gln	Arg	Leu	Glu	Ala	Leu	Gly	Thr	Gly	Trp	Glu	Glu	Leu	Gly	
321		1145		1150		1155										
323	cgc	atg	tgg	gag	agc	cgg	caa	ggc	cgc	ttg	gcc	caa	gcc	cat	gyc	3519
324	Arg	Met	Trp	Glu	Ser	Arg	Gln	Gly	Arg	Leu	Ala	Gln	Ala	His	Gly	

VERIFICATION SUMMARY  
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
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L:2256 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7